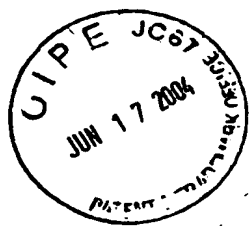


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FIG. 1A



1 CGGACGCGTGGGCGCGCAGCCTGGCTGACCTGATCCTGGACCAGTGCCCCGACCGCGGCG 60
 61 CGCCGGTGCCGCGAGATGCTGGCCCAGCCGAGCGGCTGCTCTTCATCCTGGACGGCGCGG 120
 1 M I A Q P Q R L I F I L D G A D 16
 121 ACGAGCTGCCGGCGCTGGGGGGCCCCGAGGCCGCGCCCTGCACAGACCCCTTCGAGGCGG 180
 17 E L P A L G G P E A A P C T D P F E A A 36
 181 CGAGCGGCGCGCGGGTGCTAGGCGGGTGCTGAGTAAGGCGCTGCTGCCCACGGCCCTCC 240
 37 S G A R V I G G I I S K A L I P T A L L 56
 241 TGCTGGTGACACGCGCGCCGCCCGCCCCGGGAGGCTGCAGGGCCGCTGTGTTCCTCCGC 300
 57 I V T T R A A A P G R I Q G R L C S P Q 76
 301 AGTGCGCCGAGGTGCGCGGCTTCTCCGACAAGGACAAGAAGAAGTATTTCTACAAGTTCT 360
 77 C A E V R G F S D K D K K K Y F Y K F F 96
 361 TCCGGGATGAGAGGAGGGCCGAGCGCGCTACCGCTTCGTGAAGGAGAACGAGACGCTGT 420
 97 R D E R R A E R A Y R F V K E N E T I F 116
 421 TCGCGCTGTGCTTCGTGCCCTTCGTGTGCTGGATCGTGTGCACCGTGCTGCGCCAGCAGC 480
 117 A I C F V P F V C W I V C T V I R Q Q L 136
 481 TGGAGCTCGGTGCGGACCTGTGCGGCACGTCCAAGACCACCACGTACGTGTACCTGCTTT 540
 137 E L G R D L S R T S K T T T S V Y I L F 156
 541 TCATCACCAGCGTTCTGAGCTCGGCTCCGGTAGCCGACGGGCCCCGGTTGCAGGGCGACC 600
 157 I T S V L S S A P V A D G P R L Q G D I 176
 601 TGC GCAATCTGTGCCGCTGGCCCCGCGAGGGCGTCCTCGGACGCGAGGGCGCAGTTTGCCG 660
 177 R N I C R I A R E G V L G R R A Q F A E 196
 661 AGAAGGAACCTGGAGCAACTGGAGCTTCGTGGCTCCAAAGTGCAGACGCTGTTTCTCAGCA 720
 197 K E I E Q L E L R G S K V Q T L F L S K 216
 721 AAAAGGAGCTGCCGGGCGTGCTGGAGACAGAGGTCACCTACCAGTTCATCGACCAGAGCT 780
 217 K E L P G V L E T E V T Y Q F I D Q S F 236
 781 TCCAGGAGTTCCTCGCGGCACCTGTCTACCTGCTGGAGGACGGCGGGGTGCCAGGACCG 840
 237 Q E F L A A L S Y L I E D G G V P R T A 256
 841 CGGCTGGCGGCGTTGGGACACTCCTGCGTGCGGACGCCGACCGCACAGCCACTTGGTG 900
 257 A G G V G T L I R G D A Q P H S H L V L 276

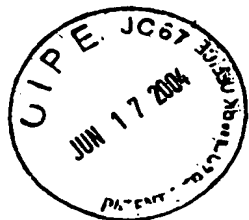


FIG. 1B

901 TCACCACGCGCTTCCTCTTCGGACTGCTGAGCGCGGAGCGGATGCGCGACATCGAGCGCC 960
277 T T R F L F G L L S A E R M R D I E R H 296

961 ACTTCGGCTGCATGGTTTCAGAGCGTGTGAAGCAGGAGGCCCTGCGGTGGGTGCAGGGAC 1020
297 F G C M V S E R V K Q E A L R W V Q G Q 316

1021 AGGGACAGGGCTGCCCCGGAGTGGCACCAGAGGTGACCGAGGGGGCCAAAGGGCTCGAGG 1080
317 G Q G C P G V A P E V T E G A K G L E D 336

1081 ACACCGAAGAGCCAGAGGAGGAGGAGGAGGGAGAGGAGGCCAACTACCCACTGGAGTTGC 1140
337 T E E P E E E E E G E E P N Y P L E L L 356

1141 TGTACTGCCTGTACGAGACGCAGGAGGACGCGTTTGTGCGCCAAGCCCTGTGCCGTTCC 1200
357 Y C L Y E T Q E D A F V R Q A L C R F P 376

1201 CGGAGCTGGCGCTGCAGCGAGTGCCTTCTGCCGCATGGACGTGGCTGTTCTGAGCTACT 1260
377 E L A L Q R V R F C R M D V A V L S Y C 396

1261 GCGTGAGGTGCTGCCCTGCTGGACAGGCACTGCGGCTGATCAGCTGCAGATTGGTTGCTG 1320
397 V R C C P A G Q A L R L I S C R L V A A 416

1321 CGCAGGAGAAGAAGAAGAGCCTGGGGAAGCGGCTCCAGGCCAGCCTGGGTGGCGGCA 1380
417 Q E K K K K S L G K R L Q A S L G G G S 436

1381 GTTCTCAAGGCACCACAAAACAAGTCCAGCCTCCCTTCTTCATCCACTCTTTCAGGCAA 1440
437 S Q G T T K Q L P A S L L H P L F Q A M 456

1441 TGA CTGACCCACTGTGCCATCTGAGCAGCCTCACGCTGTCCCACTGCAA ACTCCCTGACG 1500
457 T D P L C H L S S L T L S H C K L P D A 476

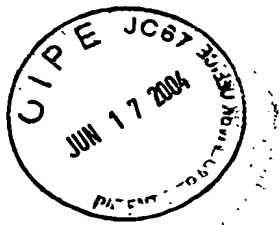
1501 CGGTCTGCCGAGACCTTTCTGAGGCCCTGAGGGCAGCCCCGCACTGACGGAGCTGGGCC 1560
477 V C R D L S E A L R A A P A L T E L G L 496

1561 TCCTCCACAACAGGCTCAGTGAGGCGGGACTGCGTATGCTGAGTGAGGGCCTAGCCTGGC 1620
497 L H N R L S E A G L R M L S E G L A W P 516

1621 CGCAGTGCAGGGTGCAGACGGTCAGGGTACAGCTGCCTGACCCCAGCGAGGGCTCCAGT 1680
517 Q C R V Q T V R V Q L P D P Q R G L Q Y 536

1681 ACCTGGTGGGTATGCTTCGGCAGAGCCCCGCCCTGACCACCTGGATCTCAGCGGCTGCC 1740
537 L V G M L R Q S P A L T T L D L S G C Q 556

1741 AACTGCCCCGCCCCATGGTGACCTACCTGTGTGAGTCTGCAGCACCAGGGATGCGGCC 1800
557 L P A P M V T Y L C A V L Q H Q G C G L 576



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FIG. 1C

1801 TGCAGACCCTCAGTCTGGCCTCTGTGGAGCTGAGCGAGCAGTCACTACAGGAGCTTCAGG 1860
577 Q T S A S V E S E Q S L Q E Q A 596

1861 CTGTGAAGAGAGCAAAGCCGGATCTGGTCATCACACACCCAGCGCTGGACGGCCACCCAC 1920
597 V K R A K P D V I T H P A L D G H P Q 616

1921 AACCTCCCAAGGAAGTCACTCTCGACCTTCTGAGGCTCTGGTGGCCAGAGCAGGCTGGAAG 1980
617 P P K E L I S T F 625

1981 ACCCTAGTCAAAGTCCCTGTGGAGAGAACGGCCCATTCGAAGGGCAGGAGGATATTGCTC 2040

2041 TCGGCCTTTGGGAAACTTTTGAGCCGAGAGGCCGAGACAGGCATGTGGGAGGCCAGAC 2100

2101 ACGGCACCCTGCCCCGTCCAGGACAGGCCAGGACCTGCCCTCTCTCCACACCTGGGGT 2160

2161 ACCCCTTCTCCCCAGCCCCACCACTACTCCACCCACCTTCTCTCCTGAGACCCTCCAG 2220

2221 CCATTCCCCTTGAAAAACCCCCCGACCCCAAGCCACAATAATGACAGCGAGAGCTCCAA 2280

2281 TTAAC TAAGCACCTACCTGGCGGCAGAATAACCCTTCACTGCCTGATCCCCATCTGCAGT 2340

2341 GTGGCCCAACAGCCCCCAGAACTATGCCCACATAGACTGGAGGTAGGCAGTTCACCGTCC 2400

2401 CTCCCTGTTAGGAATGAGACCATCCCTGAGGCTATGGCCAGGCCACAGGCGTCCAGTG 2460

2461 TCTGAGATCTTTGGGAAGGGAGACTAGGGCAGGTGGAGACAGCGCAGAACCCCGTGCTG 2520

2521 GGTGGGAAGCATGACCACATGGTGGGTGAGCAGCCCCCATGCACTGACGGTAAATTCCCC 2580

2581 TGTGGACTCATTCTGTGTTGTTTCTATTACACCTGGCCAGGCGTGGTACAATACAGGTCG 2640

2641 GTGCTCACAAA 2689

FIG. 2A-1

		1	50
HLRRSI1		(1)	-----
caspase_recruitment_protein		(1)	MAGGAWGR L ACYLEFLIKKEELKEFOLLLANKAHSRSSSGETPAQPEKTESG
cryopyrin		(1)	-MASTRCK L ARYLEDLEDVDLKKFKMHLEDYPPQKGCIPLP R GQTEKADH
Nucleotide_Binding_site		(1)	---MGFN L QALL E Q L LSQDEL S KFKY L ITTESPAH E LQ K TPHKEVDKADG
		51	100
HLRRSI1		(1)	-----
caspase_recruitment_protein		(51)	MEVAS Y LVAQYCEQ R AWMD L ALH T WEQ M GLR S LCAQ A QEGAGH S PSFP Y SP
cryopyrin		(50)	V D L A TL M IDFN G EE K AWA M AM W IFAA T NR R DL Y E K A R DEPK W CS D NARV
Nucleotide_Binding_site		(47)	K Q LVE L IT T HCD S Y W WEMAS L QVFEK M HRMD L SERAK D EVREA L KS E NK
		101	150
HLRRSI1		(1)	-----
caspase_recruitment_protein		(101)	SEPHLGSPSQPTSTAVLMPWIHELPA G CTQGSERRVLRQLPDTSGRRWRE
cryopyrin		(100)	SN -----
Nucleotide_Binding_site		(97)	RK-----

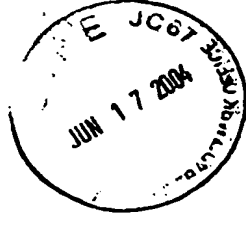


FIG. 2A-2

	151		
HLRRII1	(1)	-----	200
caspase_recruitment_protein	(151)	ISASHLYQALPSSPDHESPSPQESNAPTSTAVLGSWGSPQP	PSIAPREQE
cryopyrin	(102)	-----	PLVTCQEDS
Nucleotide_Binding_site	(99)	-----	PLSLGITR-
	201		250
HLRRII1	(1)	-----	
caspase_recruitment_protein	(201)	APGTQWPLDETSGIYYTEIREREREREKSEKGRPPMAAVVGITPPQAHSSIQP	
cryopyrin	(111)	IEEWMGLLEYLEYLSRISICKMKKDYRKKYVRSRFQCIEDRNARLGESV	
Nucleotide_Binding_site	(107)	KERPPIIDVDEMLERFKTEAQDKDNRCRYILKTKFEREMWKSWPGDSKEVQV	
	251		300
HLRRII1	(1)	-----	
caspase_recruitment_protein	(251)	HHHPWEPSVRESLCSTWPWKNEEDFNQKFTQLLLQRP	PHPRSQDPLVKRSW
cryopyrin	(161)	SLNRYTRRLRIKEHRSQQEREQELLAIGTKTKCESPV	-----
Nucleotide_Binding_site	(157)	MAERXKMLIPFSNPR	-----



FIG. 2A-3

		301			350
HLRRSI1	(1)	---		---	
caspase_recruitment_protein	(301)	PDVVEENRGH	IEIRD	LFPG	LDIQEPRIVLQGAAGIGKSTLARQVKEA
cryopyrin	(199)	-----SP	KMELLFDP	DDHSEPV	HTVVFOGAAGIGKTIILARKMMLD
Nucleotide_Binding_site	(172)	-----	VLPG	PFSY	TVVLYGPAAGLGKTTLAQKLM
		351			400
HLRRSI1	(1)	---		---	MLA
caspase_recruitment_protein	(351)	WGRGQLYG	DRFQHFVYF	ESCRELAQ	SKVVSIAELIGKDGATAPAPIRQILS
cryopyrin	(241)	WASGILYQ	DRFDYLFYH	CHREVS	LVLTQRSIGDLIMSCCPDPNPPHKTIVR
Nucleotide_Binding_site	(202)	WAE	DNLIHK-FK	YAFYLS	CRELSRGLGPCSFAELVFRDWPELQDDIPHILA
		401			450
HLRRSI1	(4)	QPQRLLF	ILDGAD	ELP-ALG	CPPEAAPCTDPPFAASGARVLCGLLSKALLP
caspase_recruitment_protein	(401)	RPERLLF	ILDGVDE	PCWVLQ	EPSSELCLHNSQPQPADALLGSLIGKTIIP
cryopyrin	(291)	KPSRI	LF	MDGFDELQ	CAFEDEHICPLCTDWQKAERGDIISLIRKKLLP
Nucleotide_Binding_site	(251)	QARKKLF	VIDGFDELG	NA	PGALIEDICGDWEKKKFPVPLIGSLINRVM

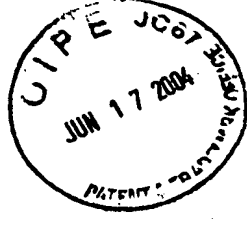
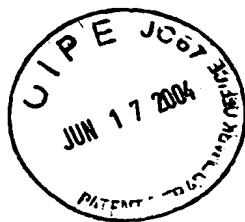


FIG. 2A-4



			451				500
			(53)	TALLVTTTRAAAPCRLOGRICSPQCAEVRGFSDDKDKKKYFYKFFRDERRA			
	HLRRSI1		(451)	EASLLITARTTALQNLIPSLQARWVEVLGFSESSRKEYFYRYFTDERQA			
	caspase_recruitment_protein		(341)	EASLLITTRPVALEKQLHLIDHPRHVELLGFSEAKRKEYFFKYSDEAQA			
	cryopyrin		(301)	KAAALLVTRPRALRDLRILAEETPIYRVEGFLFEEDKRAYFLRHFGEDEDA			
	Nucleotide_Binding_site						
			501				550
			(103)	ERAYRIVKENETLFALCFVPEVCWIVCTVLRQQEELGRDLSTRTSKTTTSV			
	HLRRSI1		(501)	IRAFRLVKSNEKELWALCTVPWVSMFACTCLMQQMKRKEKLTLTSTKTTTTL			
	caspase_recruitment_protein		(391)	RAAFSLIOENEVLFATMCFHPLVCWIVCTGLKQQMESGKSLAOTSKTTTAV			
	cryopyrin		(351)	MRAFELMRSNAALFQLGSAPAVCWIVCTTLKLQMEKGEDPVPTCLTRTGL			
	Nucleotide_Binding_site						
			551				600
			(153)	YLLFITSVLSSAPVADGCPRLQCDLRNLCRLAREGVLRRAQFAEKELEQL			
	HLRRSI1		(551)	CLHMLAQALQAP-----LGPQLRDLCSLAAEGIWQKTLFSPDDIRKH			
	caspase_recruitment_protein		(441)	YVFFLSSLQPRGGSQEHGLCAHLWGLCSLAAADGIWNNOKILFEE\$DLRNH			
	cryopyrin		(401)	ELRFLCSREP-----QCAQLRCALRTL\$LLAAQGLWAQTSVLRHREDI\$RL			
	Nucleotide_Binding_site						

FIG. 2B-1

		601			650
HLRSI1		(203)	ELRCSKVQTLFLSKKELPGVLETEVTYQFIDQSFQEFLLAALSYLEDDGGV		
caspase_recruitment_protein		(595)	GLDCAITSTFLKMG--ILQEHPIPLSYSFHLCQFQEFFAAMSIVLEDEK-		
cryopyrin		(491)	GLOKADVSAFLRMN-LEQKEVDGEKFYSFIHMTFQEFFAAMYILLEEKE		
Nucleotide_Binding_site		(446)	GVQESDIERLFLDGD-ILRQDRVSKGCYSFIHLSFQQFLTALFYTLEKEEE		
		651			700
HLRSI1		(253)	PRTAAGC-----VGTLLRCDAQPHSHLMLTTRFLFGLLSAERMMD		
caspase_recruitment_protein		(642)	-----CRGKHSNCIIDLLEKTLQAYGTHGLFGASTTTRFLGLISDEGERE		
cryopyrin		(540)	GRTNVPGSRLEKLP SRDVTLLLENYCKFEKGYLIFFVWRFLFGLVNOERTSY		
Nucleotide_Binding_site		(495)	EDRDGHTWDIG---DVQKLISGVERLRNPDLIQAGYVSFGLANERAKKE		
		701			750
HLRSI1		(293)	IERHFGCMVSEPVKQEA LRWVQCGQGCGPGVAPEVTEGAKGLEDTTEEPPE		
caspase_recruitment_protein		(686)	MENIFHCRLSQ--GRNLMQWVPSL-----QLLQPHS-----		
cryopyrin		(590)	LEKLSCKISQOIRLELLKMLEVK-----AKAKKLOIQPSQ		
Nucleotide_Binding_site		(541)	LEATFGCRMSPDIKQELLRCDISC-----KCGHSTVTDLQ		



751
800

008

751 800

(343) EEEGEEPNYP LELLYCLYETQEDAFVRQALGCRFPELALQ RVRFCRMDVAV

(716) ----- LESLECLYETRNKTHLTQWAEFFEEGMC --VETDMELLV

(626) ----- LELFYCLYEMQEEEDFVQRAMDYFPKIEEN --LSTRMDHNV

(576) ----- ELLGCLYESQEEELVKEVWAQFKEISLE --LNAVVDVVP

801
(393) L S Y C V R C C P A Q A L R L I S C R L V A A Q E K K K K S L C K R L Q A S L C G C S S Q ---
(754) C T F C I K F S R H V K K L Q L I E G R O H R S T W S P S M V L F R W P V T D A Y W Q I L F S -
(664) S S F C I E N C H R V E S L S I G F L G N M P K E E E E E E K E G R L D M V C C V L P S S S E A A
(612) S S F C V K H C R N L O K M S L Q V I K E N L P E N V T A S E S D A E V E R S O D D O H M L P E W T 850

851
(439)
(803)
(714)
(662)

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FIG. 2B-3

		901			950
		(439)	HLRRSI1	-----CITKQLPASLLELLELFOAMTDPLCELSSLT	
	caspace_recruitment_protein	(803)		-----VLKVRNLIKELDLSGNSLSHSAVKS LCKTTLRRPRCLLETLR	
	cryopyrin	(725)		SSFCRGLFSLVSTQSLELDLSDNSLGDPCMRVLCETLQHPGCNIRRLW	
	Nucleotide_Binding_site	(712)		PADAHRNLCTALRCHKTVTYLTLOQNDQDDMEFPALCEMLRHPCCNLRVLG	
		951			1000
	HLRRSI1	(468)		LSHCKLPDAVCRDLSEALRAAPALTTELCLLENRLSEAGLRMLSEGLAWPQ	
	caspace_recruitment_protein	(844)		LACGLTAEDCKDLAFGLRANOTLTELDLSFNVLMDAGAKHLCCQRLRQPS	
	cryopyrin	(775)		LGRCLGHECCFDISLVLSNQKLVELDLSDNALGDFGIRLLCVGLKHL	
	Nucleotide_Binding_site	(762)		LVSCSATQQWADLSALEVNOQLTCVNLSDNELDEGAKLLYTTLRHPK	
		1001			1050
	HLRRSI1	(518)		CRVQTVRVLQLPDPQ-RGLQYLVCMLRQSPALTTLDLSCCQLPAPMVTYLC	
	caspace_recruitment_protein	(894)		CKLQRLQLVSCGLTSDCCQDLASVLASPSLKELDLQNNLDDVGVRLC	
	cryopyrin	(825)		CNLKLLWLVSCCLTSACCDLASVLSTSHSLRLYVGENALGD\$GVAI LC	
	Nucleotide_Binding_site	(812)		CFLQRLSLENCHLTFAKCKDLAAVIVVSRLELTHLCLAKNPICNTGVKELC	

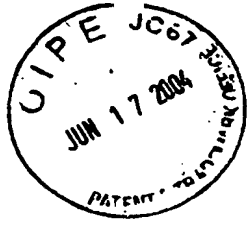


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FIG. 2B-4

HLRRSI1	1051	1100
caspase_recruitment_protein	(567) AVLQHQCCLQTLSLASVELSEQSLQELQAVKRAKPDILVITTEPALDGHPO	
cryopyrin	(944) EGLRHPAACKLIRLGLDQITLSDEMRQELRALEQEKQQLLI FSRRKPSVMT	
Nucleotide_Binding_site	(875) EKAKNPQCNLQKLGIVNSGLTSVCCSALSSVLSTNQNLTHLYLRGNTLGD	
	(862) EGLRYPECKLQTLVLMWNCBITSDGCCDLTKLQEKSSLLCLDLGNHIGV	
HLRRSI1	1101	1150
caspase_recruitment_protein	(617) PPKELISTF-----	
cryopyrin	(994) PIEGLDTGEMSNSTSSIKRQRLGSERAASHVAQANLKLIDVSKIETPIAET	
Nucleotide_Binding_site	(925) KGIKLLCEGLLHPDCKLQVLELDNENITSHCCWDLSITLLTSQSRLKLSL	
	(912) KGMKFLCEALRKPLCNLRCLWLWGCSTPPFSCEDICSALSN-QSLVTLDL	
HLRRSI1	1151	1200
caspase_recruitment_protein	(626) -----	
cryopyrin	(1044) AEFSSPEVVPVELTCVPSPASQGLHTKPLGLTDDDEWGCTGVPVATEVVDK	
Nucleotide_Binding_site	(975) GNN---DLGDLGVMMFCEVLKQSSCLLQNLGLSEMNFNYETKSALETLOE	
	(961) GQN---PLGSSGVKMMFEETLTCSSGTLRTIRLKIDDFENDELNKLLEETEE	





HLRRSI1	(626)	-----	1201	1250
caspase_recruitment_protein	(1094)	EKNLYRVHFPVAGS MRWPN IGLCF WV REAVTVEIEFCVWDQFLGEINPQH		
cryopyrin	(1022)	EKPELTIVFEP SW		
Nucleotide_Binding_site	(1008)	KNPQLIITDTEKHH PWA ERP SS HDF ML		
			1251	1300
HLRRSI1	(626)	-----		
caspase_recruitment_protein	(1144)	SWMVAGPLLDIKAEPGAVEAVHLPHFVALQGGHVDTSLFQVAHFKEEGML		
cryopyrin	(1035)	-----		
Nucleotide_Binding_site	(1034)	-----		
			1301	1350
HLRRSI1	(626)	-----		
caspase_recruitment_protein	(1194)	LEKPARVELHHIVLENPFSPLGVLLKMIHNALRFIPVTSVVLVYHRLHP		
cryopyrin	(1035)	-----		
Nucleotide_Binding_site	(1034)	-----		

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FIG. 2C-2

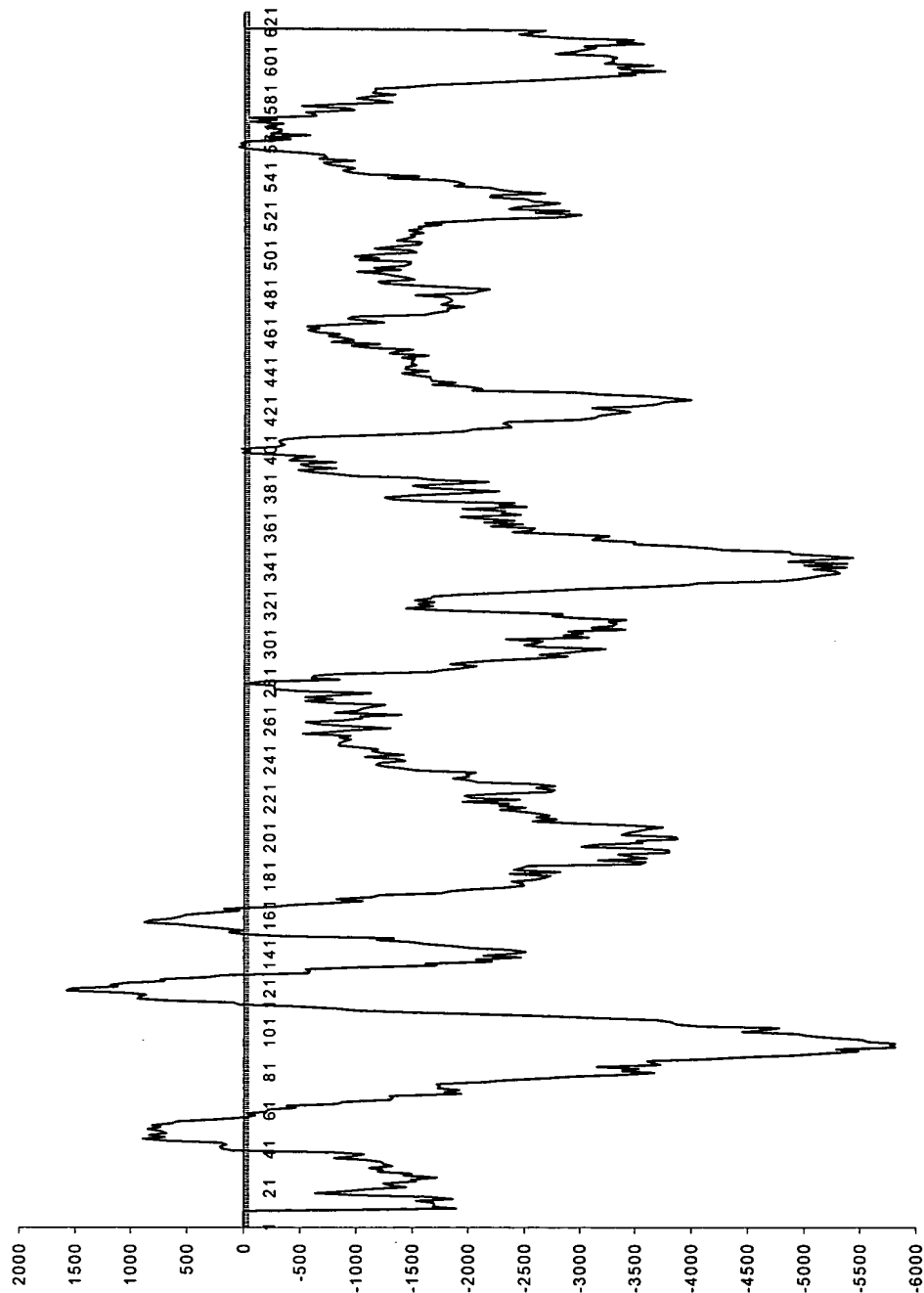
HLRRSI1	1351		1400
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1244)	EEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVGHLSGIRLQVK	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----
HLRRSI1	1401		1450
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1294)	DKKDETLVWEALVKGDLMPATTLIPPACIAVPSPLDAPQLLHFVDQYRE	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----
HLRRSI1	1451		1500
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1344)	QLIARVTSVEVVLDKLGQVLSQEYQYERVLAEENTRPSQMRKLFSLSQSWD	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----
HLRRSI1	1501		1536
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1394)	RKCKDGLYQALKETHPHLIMELWEKSKKGLPLSS	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----



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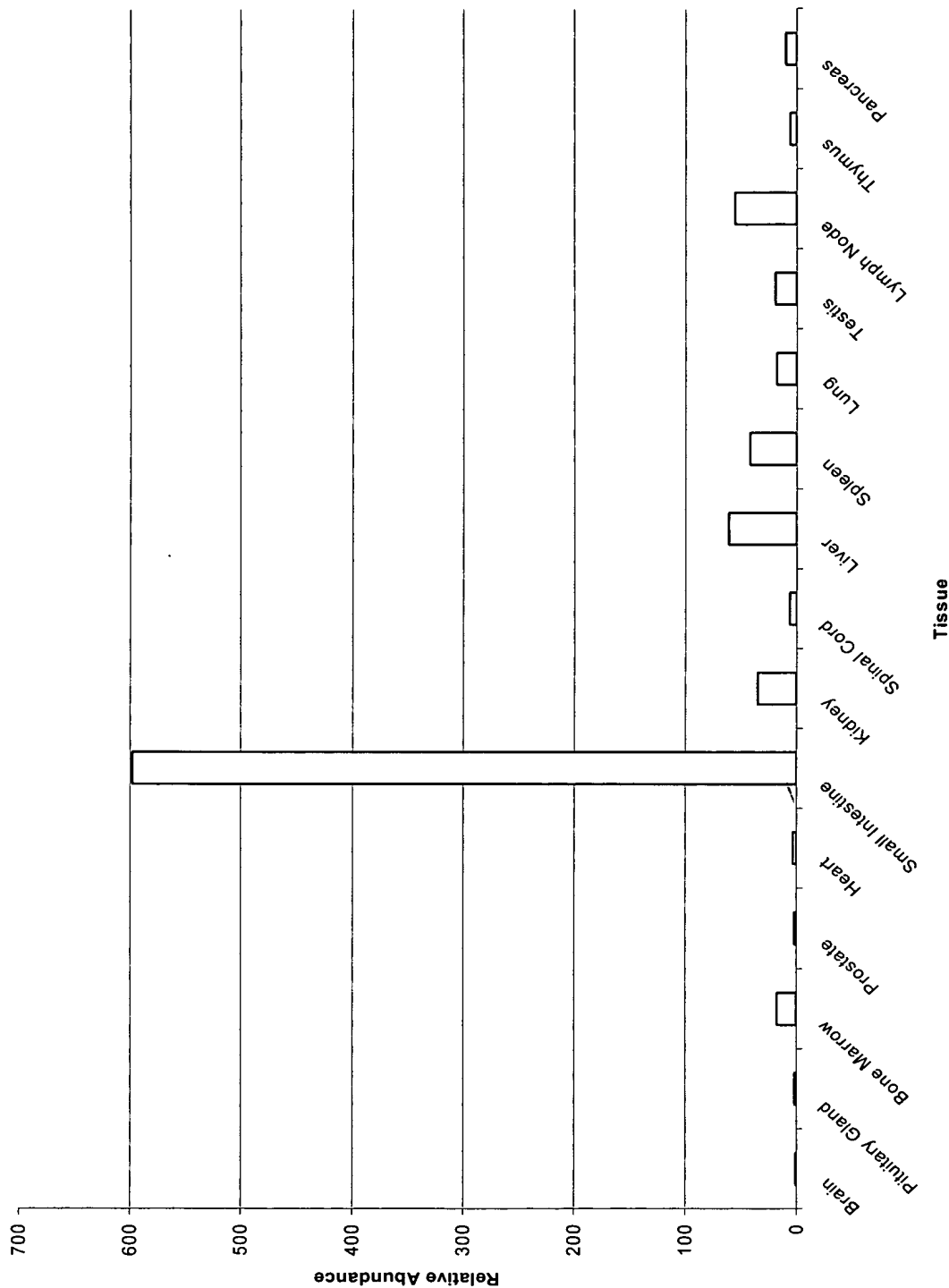
FIG. 3



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FIG. 4





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FIG. 5

Protein	Genbank ID	Identities	Similarities
human caspase recruitment protein 7	gi 10198209	36.3%	44.0%
human nucleotide binding site protein	gi 10198207	35.0%	42.2%
human cryopyrin protein	gi 17027237	35.7%	46.0%